

Gencore version 4.5
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OM protein - protein search, using sw model

Run on: March 1, 2001, 16:22:06 ; Search time 88.16 Seconds

(without alignments)

38.555 Million cell updates/sec

Title: US-09-331-631A-33
Perfect score: 77
Sequence: 1 CAXCXXXCXXXXXXXXXCAAXXXC 29

Scoring table: BLOSUM62DX Gapop 10.0 , Gapext 0.5

Searched: 374700 seqs, 117207915 residues

Total number of hits satisfying chosen parameters: 374700

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : SPTREMBL_15:*

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phage:*
- 10: sp_plant:*
- 11: sp_reptile:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	77	100.0	43	5	Q9VDN2
2	77	100.0	49	5	Q9VDN2
3	77	100.0	49	5	Q9VDN2
4	77	100.0	152	5	Q9VDN2
5	77	100.0	164	5	Q9VDN2
6	77	100.0	188	5	Q9VDN2
7	77	100.0	273	5	Q9VDN2
8	77	100.0	314	5	Q9VDN2
9	77	100.0	325	2	Q9VDN2
10	77	100.0	625	10	Q9VDN2
11	77	100.0	109	5	Q9VDN2
12	77	100.0	666	10	Q9VDN2
13	68	88.3	39	13	Q9VDN2
14	68	88.3	46	4	Q9VDN2
15	68	88.3	62	10	Q9VDN2
16	68	88.3	72	5	Q9VDN2
17	68	88.3	73	10	Q9VDN2
18	68	88.3	74	5	Q9VDN2
19	68	88.3	75	5	Q9VDN2

RESULT	1	ALIGMENTS
RX	09VDN2	Q9sg42 arribidopsis
RA	Q9vdn2	Q9jm45 mus musculu
RA	Q9vdn2	Q90248 bombyx bom
RA	Q9vdn2	Q80641 rabidopsis
RA	Q9vdn2	Q88459 mus musculu
RA	Q9vdn2	Q9134 fragaria an
RA	Q9vdn2	Q88939 arabidopsis
RA	Q9vdn2	Q65313 latvatera th
RA	Q9vdn2	Q65066 pinea maria
RA	Q9vdn2	Q43615 petunia hyp
RA	Q9vdn2	Q91450 salvelinus
RA	Q9vdn2	Q9rl4 arabidopsis
RA	Q9vdn2	Q82328 streptomyce
RA	Q9vdn2	Q14564 homo sapien
RA	Q9vdn2	Q9liu5 oryza sativ
RA	Q9vdn2	Q9iar5 fugu rubrip
RA	Q9vdn2	Q28583 ovis aries
RA	Q9vdn2	Q9n018 macropus eu
RA	Q9vdn2	Q64507 mus musculus
RA	Q9vdn2	Q19919 caenorhabdi

RA Mount S.M., Moy M., Murphy B., Murphy L., Muony D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon S., Nusslein-Volhard P., Paclob J.M.,
 RA Palazzo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svirkas R., Tector C., Turner R., Venter J.C., Wang A.-H., Wang X.,
 RA Wang Z.-Y., Wasserman D.A., Weinstock G.M., Weissbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhou W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venetian J.C.;
 RT "The genome sequence of *Drosophila melanogaster*.";
 RL Science 287: 2185-2195 (2000).
 DR EMBL: AE003730; AAFF57581; -.
 DR FLYBASE: FBgn0038790; CG5097.
 DR INTERPRO: IPR000561; -.
 DR INTERPRO: IPR000966; -.
 DR PFAM: PF0067; Metallothionein_5; 1.
 DR PRINTS: PS00872; MTDPTERA.
 DR PROSITE: PS00022; EGFL1; UNKNOWN_1.
 SQ SEQUENCE: 43 AA; 4597 MW; B54E72B14B89DFE CRC64;

Query Match 100.0%; Score 77; DB 5; Length 43;
 Best Local Similarity 20.7%; Pred. No. 6 6; Mismatches 0; Indels 0; Gaps 0;
 Matches 6; Conservative 23; Mismatches 0; Indels 0; Gaps 0;

OY 1 CXXCXXXCXXXXXXXXXXXXXXCXXC 29
 Db 3 CKGGTNCCKCDTKCGDNACNQDCRVC 31

RESULT 2
 ID 023947 PRELIMINARY; PRT; 49 AA.
 AC 023947;
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
 DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
 DE TESTIS-SPECIFIC RNA.
 GN DHTC3.
 OS Drosophila hydei (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Phylloptera; Diptera; Brachycera; Muscomorpha;
 OC Ephydriidae; Diptera; Brachycera;
 OC NCBI_TaxID:7224;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Kuech A., Buenemann H.;
 RL Submitted (DEC-1990) to the EMBL/genBank/DBJ databases.
 DR EMBL: X58114; CAA41171; -.
 DR FLYBASE: FBgn0015096; Dhyd\MS78Fa.
 DR INTERPRO: IPR001450; -.
 DR PROSITE: PS00198; 4PE4S_FERREDOXIN; UNKNOWN_1.
 DR SEQUENCE: 49 AA; 4610 MW; BE15BFEC51369F01 CRC64;

Query Match 100.0%; Score 77; DB 5; Length 49;
 Best Local Similarity 20.7%; Pred. No. 7 1; Mismatches 0; Indels 0; Gaps 0;
 Matches 6; Conservative 23; Mismatches 0; Indels 0; Gaps 0;

OY 1 CXXCXXXCXXXXXXXXXXXXXXCXXC 29
 Db 3 CGPCGCCGPGCCGCPYSCCGPYSCC 31

RESULT 3
 ID 023948 PRELIMINARY; PRT; 49 AA.
 AC 023948;
 DT 01-Nov-1996 (TREMBLrel. 01, Created)
 DT 01-Nov-1996 (TREMBLrel. 01, Last sequence update)

Query Match 100.0%; Score 77; DB 5; Length 49;
 Best Local Similarity 20.7%; Pred. No. 7 1; Mismatches 0; Indels 0; Gaps 0;
 Matches 6; Conservative 23; Mismatches 0; Indels 0; Gaps 0;

OY 1 CXXCXXXCXXXXXXXXXXXXXXCXXC 29
 Db 3 CGPCGCCGPGCCGCPYSCCGPYSCC 31

RESULT 4
 ID 09XVX3 PRELIMINARY; PRT; 152 AA.
 AC 09XVX3;
 DT 01-NOV-1999 (TREMBLrel. 12, Created)
 DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)
 DT 01-MAY-2000 (TREMBLrel. 13, Last annotation update)
 DE C06A16 PROTEIN.
 GN C06A16.
 OC Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
 OC Rhabditidae; Peioderinae; Caenorhabditis.
 OC NCBI_TaxID:6239;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=94150718; PubMed=7906398;
 RA Monmrey A.;
 RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of *C. elegans*";
 RT Submitted (JUN-1995) to the EMBL/GenBank/DBJ databases.
 RL SEQUENCE FROM N.A.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=94150718; PubMed=7906398;
 RA Wilson R., Ainscough R., Anderson K., Baynes C., Berks M.,
 RA Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,
 RA Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L.,
 RA Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,
 RA Jones M., Kershaw J., Kirstein J., Laister N., Latreille P.,
 RA Lightning J., Lloyd C., Monmrey A., Mortimore B., O'Callaghan M.,
 RA Parsons J., Percy C., Riken L., Roopra A., Saunders D., Showken R.,
 RA Smalton N., Smith A., Soinhammar E., Stedan R., Sulston J.,
 RA Thivierge-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R.,
 RA Watson A., Weinstock L., Wilkinson-Sproat J., Wohldman P.,
 RA "2.2 Mb of contiguous nucleotide sequence from chromosome III of *C. elegans*";
 RA Nature 368:32-37 (1994).
 RL EMBL: Z49886; CAA90055.1; -.
 DR INTERPRO: IPR000561; -.
 DR INTERPRO: IPR001450; -.
 DR INTERPRO: IPR001502; -.
 DR PROSITE; PS00022; EGFL1; UNKNOWN_1.
 DR PROSITE; PS00198; 4PE4S_FERREDOXIN; UNKNOWN_1.
 DR PROSITE; PS0074; ENDONUCLEASE_III_1; 1.
 DR PROSITE; PS01208; VNFC; UNKNOWN_1.

RA Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,
 RA Lightning J., Lloyd C., McMurray A., Mortimore B., O'Callaghan M.,
 RA Parsons J., Percy C., Riffen L., Roopra A., Saunders D., Shownkeen R.,
 RA Watson D.N., Smith A., Sounhamer E., Staden R., Sulston J.,
 RA Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R.,
 RA Watson A., Weinstock L., Wilkinson-Sproat J., Wohldman P.;
 RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
 RL elegans.";
 RN Nature 368:32-38(1994).
 [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BRISTOL N2;
 RA Leimbach D.;
 RL Submitted (JAN-1996) to the EMBL/GenBank/DDJB databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BRISTOL N2;
 RA Waterston R.;
 RL Submitted (APR-1997) to the EMBL/GenBank/DDJB databases.
 DR EMBL; U046575; AAB52645.1; -;
 SQ SEQUENCE 273 AA; 29231 MW; 11542812CC566530 CRC64;
 RESULT 8
 Q23390 PRELIMINARY; PRT; 314 AA.
 AC Q23390;
 DT 01-NOV-1996 (T=EMBLrel. 01, Created)
 DT 01-NOV-1996 (T=EMBLrel. 01, Last sequence update)
 DE ZK1057.7. PROTEIN
 GN K1057.7.
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
 OC Rhabditidae; Rhabdinae; Caenorhabditis;
 OC NCBI-TaxID=6239;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Thomas K.;
 RL Submitted (MAR-1996) to the EMBL/GenBank/DDJB databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 MEDLINE=94150718; PubMed=7906398;
 RX Wilson R., Ainscough R., Anderson K., Baynes C., Berks M., Berks M.,
 RA Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,
 RA Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L.,
 RA Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,
 RA Jones M., Kershaw J., Kirsten J., Lalister H., Latreille P.,
 RA Lightning J., Lloyd C., McMurray A., Mortimore B., O'Callaghan M.,
 RA Parsons J., Percy C., Riffen L., Roopra A., Saunders D., Shownkeen R.,
 RA Smalton N., Smith A., Sonnhammer E., Staden R., Sulston J.,
 RA Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R.,
 RA Watson A., Weinstock L., Wilkinson-Sproat J., Wohldman P.;
 RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
 RL elegans.";
 RL Nature 368:32-38(1994).
 DR EMBL; Z/00038; CAAG93861.1; -;
 SQ SEQUENCE 314 AA; 32803 MW; 8735F50B826ED303 CRC64;

Query Match 100.0%; Score 77; DB 5; Length 314;
 Best Local Similarity 20.7%; Pred. No. 22;
 Matches 6; Conservative 23; Mismatches 0; Indels 0; Gaps 0;

OY 1 CXXCXXCXXXXXXXCCCCXCCXXC 29
 DB 105 CNQCCQCCISSCATPICAQSCNNQCSSC 133

RESULT 9
 Q083828 PRELIMINARY; PRT; 325 AA.
 ID 083828
 AC 083828;
 DT 01-NOV-1998 (T=EMBLrel. 08, Created)
 DT 01-MAY-1998 (T=EMBLrel. 08, Last sequence update)
 DT 01-MAY-2000 (T=EMBLrel. 13, Last annotation update)
 DE HYPOTHETICAL 34.1 KDA PROTEIN.
 TP0856.
 OS Treponema pallidum.
 OC Bacteria; Spirochaetales; Spirochaetaceae; Treponema.
 OX NCBI-TaxID=160;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=NICHOOLS;
 RX MEDLINE=98332770; PubMed=9665876;
 RA Fraser C.M., Norris S.J., Weinstock G.M., White O., Sutton G.G.,
 RA Dodson R., Gwinn M., Hickey E.K., Clayton R., Ketchum K.A.,
 RA Sodergren E., Hardham M.P., McLeod M.P., Salzberg S., Peterson J.,
 RA Khalak H., Richardson D., Howell J.K., Chidambaram M., Utterback T.,
 RA McDonald L., Artiach P., Bowman C., Cotton M.D., Fujii C., Garland S.,
 RA Hatch B., Horst K., Roberts K., Sandusky M., Weidman J., Smith H.O.,
 RA Venter J.C.,
 RT "Complete genome sequence of Treponema pallidum, the syphilis
 RT spirochete.";
 RL Science 281:375-388(1998);
 DR EMBL; AE001256; AAC5828.1; -.
 TIGR; TP0056; -.
 KW Hypothetical protein.
 SQ SEQUENCE 325 AA; 34054 MW; F9CFDCBD253C07D2 CRC64;

Query Match 100.0%; Score 77; DB 2; Length 325;
 Best Local Similarity 20.7%; Pred. No. 22;
 Matches 6; Conservative 23; Mismatches 0; Indels 0; Gaps 0;

OY 1 CXXCXXCXXXXXXXCCCCXCCXXC 29
 DB 238 CTKSGRCITGWGTCNGERPKCCKCDCNC 266

RESULT 10
 Q09SPL3 PRELIMINARY; PRT; 625 AA.
 ID 09SPL3
 AC 09SPL3;
 DT 01-MAY-2000 (T=EMBLrel. 13, Created)
 DT 01-MAY-2000 (T=EMBLrel. 13, Last sequence update)
 DT 01-OCT-2000 (T=EMBLrel. 15, Last annotation update)
 DE VICILIN PRECURSOR (FRAGMENT).
 GN AMP2.
 OS Macadamia integrifolia (Macadamia nut).
 OC Eukaryota; Viridiplanteae; Embryophyta; Tracheophyta; Spermatophyta;
 OC Magnoliopsida; eudicotyledons; Proteaceae; Macadamia.
 OX NCBI-TaxID=60698;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-NUT Kernel;
 RA Marcus J.P., Goultier K.C., Green J.L., Manners J.M.,
 RT "A family of antimicrobial peptides is produced by processing of a 7S
 RT globulin protein in Macadamia integrifolia.";
 RL Plant J. 0:0-0(1999);
 DR EMBL; AF061885; AAD54245.1; -.
 HSSP; P02853; 2PHL.

DR INTERPRO; IPR001113; -.
 DR PFAM; PF00546; Seedstore_7s; 1.
 FT
 SEQUENCE 625 AA; 73586 MN; 415808A89B370296 CRC64;
 SQ

Query Match 100.0%; Score 77; DB 10; Length 625;
 Best local similarity 20.7%; Pred. No. 33;
 Matches 6; Conservative 23; Mismatches 0;
 Indels 0; Gaps 0;

Qy 1 CXXCXXXXXXXCXXXXCXXXCXXXC 29
 Db 41 COCORRCRQQESDPROQQYCORRCRIC 69

RESULT 11
 09SPL5 PRELIMINARY; PRT; 666 AA.
 ID 09SPL5
 AC 09SPL5;
 DT 01-MAY-2000 (TREMBREL 13, Created)
 DT 01-MAY-2000 (TREMBREL 13, Last sequence update)
 DT 01-OCT-2000 (TREMBREL 15, Last annotation update)
 DE VICTILIN PRECURSOR.
 GN AMP2.
 OS Macadamia integrifolia (Macadamia nut).
 OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
 OC Magnoliophyta; eudicotyledons; Proteaceae; Macadamia.
 OX NCBI_TaxID=60698;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-NUT KERNEL;
 RA Marcus J.P., Goultier K.C., Green J.L., Manners J.M.;
 RT "A family of antimicrobial peptides is produced by processing of a 7S
 globulin protein in Macadamia integrifolia kernels.";
 RL Plant J. 0-0-0(1999)
 DR EMBL; AF161883; RAD5244.1; -.
 DR HSSP; P02853; 2PHL.
 DR INTERPRO; IPR00113; -.
 DR PFAM; PF00546; Seedstore_7s; 1.
 DR SEQUENCE 666 AA; 78217 MN; C752BB884B2DF0224 CRC64;
 SQ [1]

Query Match 100.0%; Score 77; DB 10; Length 666;
 Best local similarity 20.7%; Pred. No. 34;
 Matches 6; Conservative 23; Mismatches 0;
 Indels 0; Gaps 0;

Qy 1 CXXCXXXXXXXCXXXXCXXXCXXXC 29
 Db 82 COQCQRRCRQQESDPROQQYCORRCRIC 110

RESULT 12
 09SPL4 PRELIMINARY; PRT; 666 AA.
 ID 09SPL4
 AC 09SPL4;
 DT 01-MAY-2000 (TREMBREL 13, Created)
 DT 01-MAY-2000 (TREMBREL 13, Last sequence update)
 DT 01-OCT-2000 (TREMBREL 15, Last annotation update)
 DE VICTILIN PRECURSOR.
 GN AMP2.
 OS Macadamia integrifolia (Macadamia nut).
 OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
 OC Magnoliophyta; eudicotyledons; Proteaceae; Macadamia.
 OX NCBI_TaxID=60698;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-NUT KERNEL;
 RA Marcus J.P., Goultier K.C., Green J.L., Manners J.M.;
 RT "A family of antimicrobial peptides is produced by processing of a 7S
 globulin protein in Macadamia integrifolia.";
 RL Plant J. 0-0-0(1999)
 DR EMBL; AF161884; RAD5245.1; -.
 DR HSSP; P02853; 2PHL.

RESULT 13
 09PGV7 PRELIMINARY; PRT; 39 AA.
 ID 09PGV7;
 AC 09PGV7;
 DT 01-MAY-2000 (TREMBREL 13, Created)
 DT 01-MAY-2000 (TREMBREL 13, Last sequence update)
 DT 01-MAY-2000 (TREMBREL 13, Last annotation update)
 DE RECEPTOR TYROSINE KINASE XMRK (FRAGMENT).
 GN XMRK.
 OS Xiphophorus maculatus (Southern platyfish).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Buteleosteii; Neoteleosteii;
 OC Acanthomorpha; Percormorpha; Atherinomorpha;
 OC Cyprinodontiformes; Poeciliidae; Xiphophorus.
 OX NCBI_TaxID=8083;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-SR;
 RX MEDLINE=99126443; PubMed=9927468;
 RA Gutbrod H.; Schartl M.;
 RT "Intragenic sex-chromosomal crossovers of Xmrk oncogene alleles affect pigment pattern formation and the severity of melanoma in Xiphophorus";
 RT Genetics 151:773-783(1999);
 RL EMBL; AF093693; RAD03714.1; -.
 KW Receptor; Kinase.
 DR NON_TER 1
 FT NON_TER 39
 SQ SEQUENCE 39 AA; 4195 MN; 42303BA05F6DB557 CRC64;

Query Match 88.3%; Score 68; DB 13; Length 39;
 Best Local Similarity 17.9%; Pred. No. 36;
 Matches 5; Conservative 23; Mismatches 0;
 Indels 0; Gaps 0;

Qy 2 XXCXXXXXXXCXXXXCXXXCXXXC 29
 Db 3 LLCAEAOCNRRRGPKPIDCCNEHCAGGC 30

RESULT 14
 016861 PRELIMINARY; PRT; 46 AA.
 ID 016861
 AC 016861;
 DT 01-NOV-1995 (TREMBREL 01, Created)
 DT 01-NOV-1996 (TREMBREL 01, Last sequence update)
 DT 01-AUG-1998 (TREMBREL 07, Last annotation update)
 DE CYSTEINE-RICH PROTEIN (FRAGMENT).
 OS Homo sapiens (Human).
 OC Mammalia; Eutheria; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Lemasson I.; Devaux C.; Messard J.M.;
 RL Submitted (JUL-1996) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; U63332; AAB05810.1; -.
 FT NON_TER 1
 SQ SEQUENCE 46 AA; 5061 MN; 311922FE40A44E8F CRC64;

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Query Match          88.3%; Score 68; DB 10; Length 62;
Best Local Similarity 17.9%; Pred. No. 47;
Matches 5; Conservative 23; Mismatches 0; Indels 0; Gaps 0
Qy      2 XXCXXXCXXXXXXXXXXXXXXXCCXXCXXC 29
Db      2 SECQORCSYRCSATSHKKPCMFQKCC 29

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Search completed: March 1, 2001, 16:22:07
Job time: 284 sec